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ART UNIT	**PAPER NUMBER**
1637	

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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

Office Action Summary	Application No.	Applicant(s)	
	10/535,629	DE HENAU ET AL.	
	Examiner	Art Unit	
	Samuel Woolwine	1637	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1)☒ Responsive to communication(s) filed on *22 August 2007*.

2a)☐ This action is **FINAL**. 2b)☒ This action is non-final.

3)☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

Disposition of Claims

4)☒ Claim(s) *1-15* is/are pending in the application.

4a) Of the above claim(s) *2 and 8-14* is/are withdrawn from consideration.

5)☐ Claim(s) _____ is/are allowed.

6)☒ Claim(s) *1,3-7 and 15* is/are rejected.

7)☐ Claim(s) _____ is/are objected to.

8)☐ Claim(s) _____ are subject to restriction and/or election requirement.

Application Papers

9)☐ The specification is objected to by the Examiner.

10)☐ The drawing(s) filed on _____ is/are: a)☐ accepted or b)☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).

11)☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

Priority under 35 U.S.C. § 119

12)☒ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a)☒ All b)☐ Some * c)☐ None of:

1.☒ Certified copies of the priority documents have been received.

2.☐ Certified copies of the priority documents have been received in Application No. _____.

3.☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

* See the attached detailed Office action for a list of the certified copies not received.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO/SB/08) Paper No(s)/Mail Date *5/20/2007*.
4) ☐ Interview Summary (PTO-413) Paper No(s)/Mail Date. _____ .
5) ☐ Notice of Informal Patent Application
6) ☐ Other: _____.

DETAILED ACTION

Priority

Receipt is acknowledged of papers submitted under 35 U.S.C. 119(a)-(d), which papers have been placed of record in the file.

Election/Restrictions

Applicant's election with traverse of Group I, claims 1-7 and 15, in the reply filed on 8/22/2007 is acknowledged. The traversal is on the ground(s) that claim 7, as amended, is not anticipated by the Fodor reference cited in the requirement for restriction (page 6 of the response). This is not found persuasive because despite the amendments to the claims in the response filed 8/22/2007, at least some claims are rejected over the prior art below. With regard to the traversal of the further requirement to elect either SEQ ID NO 1 or 2, and SEQ ID NOS related to one of these, this requirement was based on the fact that SEQ ID NOS 1 and 2 were derived from different species of *Enterococcus* (Applicant's own specification page 6, lines 30-33), and therefore lack unity of invention *a priori*. Note that Applicant has also stated that the ITS (Internal Transcribed Spacer, from which SEQ ID NOS 1 and 2 were derived) was already known for some *Enterococcus* species (specification page 6, line 7). Therefore, no prior art need have been cited to regard these sequences as lacking unity of invention. Furthermore, as outlined in the rejections over the prior art below, SEQ ID NO 1 was found within a known sequence of *Enterococcus* and is therefore considered *prima facie* obvious, thus severing any lack of unity between SEQ ID NO 1 (and SEQ ID NOS related thereto) and SEQ ID NO 2 (and SEQ ID NOS related thereto).

The requirement is still deemed proper and is therefore made FINAL.

Claims 2 and 8-14 are withdrawn from further consideration pursuant to 37 CFR 1.142(b), as being drawn to a nonelected invention, there being no allowable generic or linking claim. Applicant timely traversed the restriction (election) requirement in the reply filed on 8/22/2007.

Claim Objections

The claims recite non-elected SEQ ID NOS. Only those SEQ ID NOS elected in the response filed 8/22/2007 will be searched and examined, namely SEQ ID NOS 1, 5, 18, 34, 36 and 69. Applicant is required to remove non-elected SEQ ID NOS from the claims in response to this Office action (including replacing "Table 3" in claims 6 and 14 with the elected SEQ ID NOS therefrom).

Claim Rejections - 35 USC § 112—2nd paragraph

The following is a quotation of the second paragraph of 35 U.S.C. 112:

> The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

Claims 1 and 7 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention. Based on the wording of claim 1, it would appear that the claimed nucleic acid molecule consists of three parts (a SEQ ID NO 1 or 2, its RNA form, *and* its complementary form). Since claim 7 refers to claim 1, claim 7 could also be construed in this manner. This would not appear from the overall disclosure to be Applicant's intent. Use of alternative language (i.e. "or") would be clearer and more favorably considered.

Claim Rejections - 35 USC § 112—Written Description

The following is a quotation of the first paragraph of 35 U.S.C. 112:

> The specification shall contain a written description of the invention, and of the manner and process of making and using it, in such full, clear, concise, and exact terms as to enable any person skilled in the art to which it pertains, or with which it is most nearly connected, to make and use the same and shall set forth the best mode contemplated by the inventor of carrying out his invention.

Claims 3-7 and 15 are rejected under 35 U.S.C. 112, first paragraph, as failing to comply with the written description requirement. The claim(s) contains subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Claim 3 recites "An isolated nucleic acid of more than 10 contiguous nucleotides that specifically hybridizes to SEQ ID NO 1...". Claim 5 recites "A set of two or three polynucleotide probes...hybridizing specifically to SEQ ID NO 1...". Claim 7 simply recites "a set of two polynucleotide probes" (which do not even have to hybridize to anything).

These claims, and the claims depending therefrom, encompass an incredibly large genus of polynucleotides. In analysis of the claims for compliance with the written description requirement of 35 U.S.C. 112, first paragraph, the written description guidelines note that in regarding genus/species situations, "Satisfactory disclosure of a 'representative number' depends on whether one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed." (See: Federal Register: December 21, 1999 (Volume 64, Number 244), revised guidelines for written description.)

While SEQ ID NO 1 is 64 nucleotides in length, there are nevertheless millions of different polynucleotides that could hybridize to SEQ ID NO 1, its complementary form or its RNA form, because a polynucleotide need not exhibit 100% complementarity in order to hybridize (see for example paragraph [0025] of the published instant application). In the case of claims 3 and 5, the polynucleotides are recited to be more than 10 nucleotides in length (for claim 7 there are no limitations with regard to length). Therefore, for example, in the case of claim 3, there would be 64-11=53 perfect 11mer polynucleotides (106 when accounting for those which correspond to the complementary form of SEQ ID NO 1). However, when imperfect matches are taken into consideration, each of the 11mers could be imperfectly matched at one position (where the correct nucleotide could be replaced by one of three incorrect nucleotides): 106×11×3=3498 11mers with a single mismatch. Longer polynucleotides could tolerate more mismatches. For example, there are 92 possible perfect 18mers (accounting for SEQ ID NO 1 and its complementary form). If one calculates the number of 18mers with one mismatch: 92×18×3=4968. If each of these contains a second imperfectly matched nucleotide at one of the remaining 17 positions: 4968×17×3=253,368. The polynucleotides would also encompass those containing non-natural nucleotides, such as inosine (see paragraph [0030] of the published instant application).

Note that there is no upper length limit on the polynucleotides claimed (i.e. the polynucleotides can be longer than SEQ ID NO 1; the only requirement being that they could hybridize thereto). The number of possibilities easily extends into the hundreds of millions. Applicant's sequence listing contains 84 sequences. Assuming roughly half of

these represent primers/probes/polynucleotides capable of hybridizing to SEQ ID NO 1 (as opposed to SEQ ID NO 2), this tallies to 42 sequences to represent a genus of hundreds of millions of polynucleotides.

At some point, deviation from a perfectly matched probe will result in poorer hybridization, or none at all. However, Applicants have not defined which of the hundreds of millions of possible polynucleotides would remain hybridizable to SEQ ID NO 1, and thus has not reasonably conveyed to one of ordinary skill in the art, at the time the application was filed, that they were in possession of the entire genus of primers/probes/polynucleotides to which the claims are presently directed.

Vas-Cath Inc. v. Mahurkar, 19 USPQ2d 1111, makes clear that "applicant must convey with reasonable clarity to those skilled in the art that, as of the filing date sought, he or she was in possession of the invention. The invention is, for purposes of the written description inquiry, whatever is now claimed (See *Vas-Cath* at page 1117)." The specification does not "clearly allow persons of ordinary skill in the art to recognize that [he or she] invented what is claimed (See *Vas-Cath* at page 1116)."

The skilled artisan cannot envision the detailed chemical structure of the encompassed nucleic acids. Adequate written description requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it. The nucleic acid itself is required. See *Fiers v. Revel*, 25 USPQ2d 1601, 1606 (CAFC 1993), and *Amgen Inc. V. Chugai Pharmaceutical Co. Ltd.*, 18 USPQ2d 1016.

Finally, *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1404, 1405 held that:

> "To fulfill the written description requirement, a patent specification must describe an invention and do so in sufficient detail that one skilled in the art can clearly conclude that 'the inventor invented the claimed invention.' *Lockwood v. American Airlines, Inc.*, 107 F.3d 1565, 1572, 41 USPQ2d 1961, 1966 (1997); *In re Gosteli*, 872 F.2d 1008, 1012, 10 USPQ2d 1614, 1618 (Fed. Cir. 1989) (' [T]he description must clearly allow persons of ordinary skill in the art to recognize that [the inventor] invented what is claimed.'). Thus, an applicant complies with the written description requirement 'by describing the invention, with all its claimed limitations, not that which makes it obvious,' and by using 'such descriptive means as words, structures, figures, diagrams, formulas, etc., that set forth the claimed invention.' *Lockwood*, 107 F.3d at 1572, 41 USPQ2d at 1966.
>
> An adequate written description of a DNA, such as the cDNA of the recombinant plasmids and microorganisms of the '525 patent, 'requires a precise definition, such as by structure, formula, chemical name, or physical properties,' not a mere wish or plan for obtaining the claimed chemical invention. *Fiers v. Revel*, 984 F.2d 1164, 1171, 25 USPQ2d 1601, 1606 (Fed. Cir. 1993). Accordingly, 'an adequate written description of a DNA requires more than a mere statement that it is part of the invention and reference to a potential method for isolating it; what is required is a description of the DNA itself.' Id. at 1170, 25 USPQ2d at 1606."

Accordingly, absent a teaching of a representative number of probes hybridizable to SEQ ID NO 1, the specification provides insufficient written description to support the broadly claimed genus.

Claim Rejections - 35 USC § 102

> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

Claims 3, 5 and 7 are rejected under 35 U.S.C. 102(b) as being anticipated by Random Primer 12, sold by New England Biolabs (NEB) in the 1998/99 NEB Catalog (page 121).

By definition, this product contains every possible 12mer oligonucleotide.

The following calculations are intended to show that a vial of this prior art product contained every possible 12mer oligonucleotide, and thus every possible pair of 12mer oligonucleotides, and relies in part on the nucleic acid data of page 284 and Avogadro's number (6.02×10^{23}) describing the number of molecules in 1 mole of any substance.

Random 12-mer:

Molecular weight of 12-mer:
12×325 daltons/nucleotide = 3,900 daltons = 3,900 g/mol

Number of possible 12-mers:
$4^{12} = 1.7 \times 10^{7}$ molecules

How many molecules of 12-mer in a vial sold by NEB:
1 A_{260} unit = 33 μg = 3.3×10^{-5} g
3.3×10^{-5} g ÷ 3,900 g/mol = 8.5×10^{-9} mol
$(8.5 \times 10^{-9}$ mol) × $(6.02 \times 10^{23}$ molecules/mol) = 5.1×10^{15} molecules

How many each possible 12-mer per vial:
5.1×10^{15} molecules ÷ 1.7×10^{7} molecules = 3×10^{8}

Therefore, this prior art product *must* have contained an isolated nucleic acid molecule of more than 10 contiguous nucleotides that specifically hybridizes to SEQ ID NO 1, its RNA form, as well as its complementary form, as recited in claim 3. This product also must have contained a set of two or three polynucleotide probes which hybridize to adjacent locations on SEQ ID NO 1, its RNA form, as well as its complementary form, wherein there are no more than 25 nucleotides between said probes along the target sequence, as recited in claim 5. This product also anticipates the "or" option of claim 7, because it represents a composition comprising a set of two polynucleotide probes.

Applicant may wish to consider drafting these claims in the form of a "composition consisting of..." (and also to require something more particular about the set of two polynucleotide probes in claim 7, which in its present form does not even require the probes to be able to hybridize to any particular sequence).

Claim 7 is rejected under 35 U.S.C. 102(b) as being anticipated by Molander et al (International Endodontic Journal, vol 35, no 1, pp 1-6, January 2002, cited on the IDS of 5/20/2005).

With regard to claim 7, Molander teaches a composition comprising a set of two polynucleotide probes, said probes comprising more than 10 contiguous nucleotides (page 2, "PCR conditions", where the primers represent the claimed probes).

Claim Rejections - 35 USC § 103

The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

> (a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negatived by the manner in which the invention was made.

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

Claims 1 and 3-6 are rejected under 35 U.S.C. 103(a) as being unpatentable over Molander et al (International Endodontic Journal, vol 35, no 1, pp 1-6, January

2002, cited on the IDS of 5/20/2005) in view of GenBank® GI:1848164 [online] (publicly available 21 February 1997) [retrieved on September 3, 2007] (retrieved from the Internet: <URL:www.ncbi.nlm.nih.gov/entrez/viewer.fcgi?1848164:OLDID:3217569>) and Buck et al (BioTechniques, vol 27, pp 528-536, September 1999).

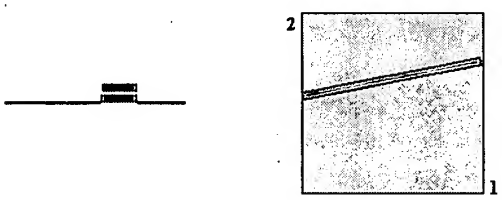
With regard to claims 1 and 3-6, Molander teaches primers comprising more than 10 contiguous nucleotides that are able to specifically hybridize to the 16S/23S rDNA intergenic region from *Enterococcus faecalis/faecium* (see abstract and page 2, "PCR conditions"). It is noted that Applicant's sequences were also derived from the 16S/23S rDNA intergenic region from *Enterococcus faecalis/faecium* (paragraph [0001]-[0003], e.g., from the published instant application).

Molander does not teach primers (or other "nucleic acid molecules") that specifically hybridize to SEQ ID NO 1, its RNA form, or its complementary form, as required by claims 3-6. Molander does not teach the specific SEQ ID NOS 1, 5, 18, 34, 36 and 69 (the elected SEQ ID NOS to which claims 1, 4 and 6 are limited; see Applicant's response submitted 8/22/2007).

However, all the recited SEQ ID NOS (including SEQ ID NO 1) can be found within a known sequence of *Enterococcus faecalis* as shown by the alignments of these SEQ ID NOS with GenBank® GI:1848164:

Sequence 1: SEQ ID NO 1
Length = 64 (1 .. 64)

Sequence 2: gi|1848164|E.faecalis 16S-23S rRNA spacer DNA & tRNA-Ala gene
Length = 328 (1 .. 328)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

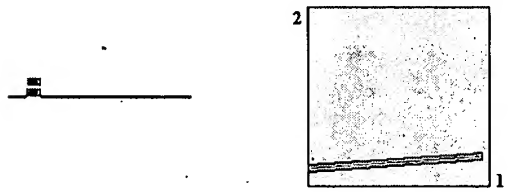
```
 Score =  123 bits (64),  Expect = 5e-26
 Identities = 64/64 (100%), Gaps = 0/64 (0%)
 Strand=Plus/Plus

Query  1    GTTCATTGAAAACTGGATATTGAAGTAAAAAGAATCAAAACAAACCGAGAACACCGCGTT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  177  GTTCATTGAAAACTGGATATTGAAGTAAAAAGAATCAAAACAAACCGAGAACACCGCGTT  236

Query  61   GAAT  64
            ||||
Sbjct  237  GAAT  240
```

Sequence 1: SEQ ID NO 5
Length = 23 (1 .. 23)

Sequence 2: gi|1848164|E.faecalis 16S-23S rRNA spacer DNA & tRNA-Ala gene
Length = 328 (1 .. 328)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

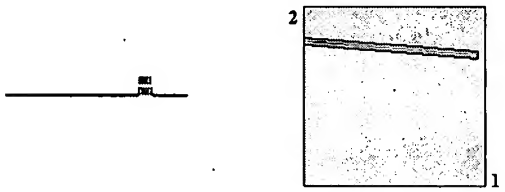
NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
 Score = 44.9 bits (23),  Expect = 0.001
 Identities = 23/23 (100%), Gaps = 0/23 (0%)
 Strand=Plus/Plus

Query  1   TACTTTGTTCAGTTTTGAGAGGT  23
           |||||||||||||||||||||||
Sbjct  35  TACTTTGTTCAGTTTTGAGAGGT  57
```

Sequence 1: SEQ ID NO 18
Length = 24 (1 .. 24)

Sequence 2: gi|1848164|E.faecalis 16S-23S rRNA spacer DNA & tRNA-Ala gene
Length = 328 (1 .. 328)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

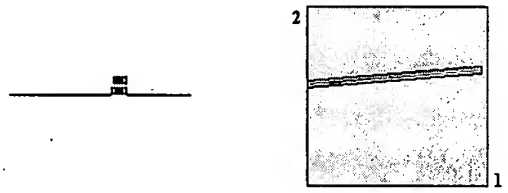
NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
 Score = 46.8 bits (24),  Expect = 5e-04
 Identities = 24/24 (100%), Gaps = 0/24 (0%)
 Strand=Plus/Minus

Query  1    GCAATTGAACTTATTAAAAAACTC  24
            ||||||||||||||||||||||||
Sbjct  264  GCAATTGAACTTATTAAAAAACTC  241
```

Sequence 1: SEQ ID NO 34
Length = 26 (1 .. 26)

Sequence 2: gi|1848164|E.faecalis 16S-23S rRNA spacer DNA & tRNA-Ala gene
Length = 328 (1 .. 328)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

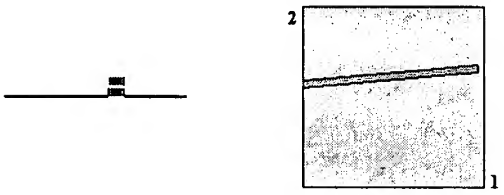
NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
 Score = 50.7 bits (26),  Expect = 6e-05
 Identities = 26/26 (100%), Gaps = 0/26 (0%)
 Strand=Plus/Plus

Query  1    AACTGGATATTGAAGTAAAAAGAATC  26
            ||||||||||||||||||||||||||
Sbjct  187  AACTGGATATTGAAGTAAAAAGAATC  212
```

Sequence 1: SEQ ID NO 36
Length = 29 (1 .. 29)

Sequence 2: gi|1848164|E.faecalis 16S-23S rRNA spacer DNA & tRNA-Ala gene
Length = 328 (1 .. 328)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

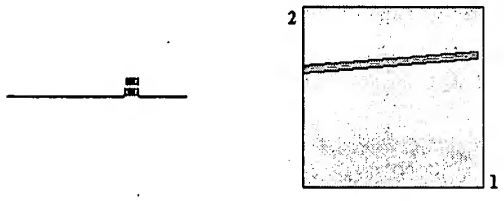
NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
 Score = 56.4 bits (29),  Expect = 2e-06
 Identities = 29/29 (100%), Gaps = 0/29 (0%)
 Strand=Plus/Plus

Query  1    CTGGATATTGAAGTAAAAAGAATCAAAAC  29
            |||||||||||||||||||||||||||||
Sbjct  189  CTGGATATTGAAGTAAAAAGAATCAAAAC  217
```

Sequence 1: SEQ ID NO 69
Length = 25 (1 .. 25)

Sequence 2: gi|1848164|E.faecalis 16S-23S rRNA spacer DNA & tRNA-Ala gene
Length = 328 (1 .. 328)



NOTE:Bitscore and expect value are calculated based on the size of the nr database.

NOTE:If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

```
 Score = 48.8 bits (25),  Expect = 2e-04
 Identities = 25/25 (100%), Gaps = 0/25 (0%)
 Strand=Plus/Plus

Query  1    ACAAACCGAGAACACCGCGTTGAAT  25
            |||||||||||||||||||||||||
Sbjct  216  ACAAACCGAGAACACCGCGTTGAAT  240
```

It would have been *prima facie* obvious to use these SEQ ID NOS as substitutes for the primers used by Molander in a method for detecting *Enterococcus*, since it was well known in the art to derive primers from a known nucleic acid sequence to amplify or

detect that same sequence. Therefore, the recited SEQ ID NOS simply represent functional equivalents to the primers taught by Molander for the purpose of amplifying/detecting *Enterococcus*. In addition, Molander provides *express* motivation to use primer pairs targeted to conserved gene sequences (last paragraph prior to "Conclusions" on page 5). This seems to be how Applicants arrived at their chosen SEQ ID NOS (see paragraph [0081] of published instant application).

Buck expressly provides evidence that one of skill in the art would have had a reasonable expectation of success in substituting the SEQ ID NOS recited in the claims for those used by Molander. Specifically, Buck invited primer submissions from a number of labs (39) (page 532, column 3), with 69 different primers being submitted (see page 530, column 1). Buck also tested 95 primers spaced at 3 nucleotide intervals along the entire sequence at issue, thereby testing more than 1/3 of all possible 18 mer primers on the 300 base pair sequence (see page 530, column 1). When Buck tested each of the primers selected by the methods of the different labs, Buck found that EVERY SINGLE PRIMER worked (see page 533, column 1). Only one primer ever failed, No. 8, and that primer functioned when repeated. Further, EVERY SINGLE CONTROL PRIMER functioned as well (see page 533, column 1). Buck expressly states "The results of the empirical sequencing analysis were surprising in that nearly all of the primers yielded data of extremely high quality (page 535, column 2)." Therefore, Buck provides direct evidence that all primers would be expected to function, and in particular, all primers selected according to the ordinary criteria, however different, used by 39 different laboratories. It is particularly striking that all 95 control primers

functioned, which represent 1/3 of all possible primers in the target region. This clearly shows that every primer would have a reasonable expectation of success.

Claim 15 is rejected under 35 U.S.C. 103(a) as being unpatentable over Molander et al in view of GenBank® GI:1848164 and Buck et al (BioTechniques, vol 27, pp 528-536, September 1999) as applied to claims 1 and 3-6 above, and further in view of the 1988 Stratagene Catalog.

The teachings of Molander, GenBank® GI:1848164 and Buck have been discussed. Since Molander teaches a PCR reaction mixture (designed to allow the primers to hybridize to their target), such a mixture can be considered a "hybridization buffer" (as recited in claim 15). These references do not teach a kit as required by claim 15.

Stratagene catalog teaches a motivation to combine reagents into kit format (page 39).

It would have been *prima facie* obvious to one of ordinary skill in the art at the time the invention of the instant application was made to package the reagents for PCR as taught by Molander in the form of a kit. Since the SEQ ID NOS 1, 5, 18, 34, 36 and 69 could all have been used as obvious primers for detecting *Enterococcus* as discussed in the rejection of claims 1 and 3-6, it would have been obvious to package them in the form of a kit, since the Stratagene catalog teaches a motivation for combining reagents of use in an assay into a kit:

"Each kit provides two services: 1) a variety of different reagents have been assembled and pre-mixed specifically for a defined set of experiments. Thus one need not purchase gram quantitites of 10 different reagents, each of which is needed in only microgram amounts, when beginning a series of experiments. When one considers all of the unused chemicals that typically accumulate in weighing rooms, desiccators, and freezers, one quickly realizes that it is actually far more expensive for a small number of users to prepare most buffer solutions from the basic reagents. Stratagene provides only the quantities you will actually need, premixed and tested. In actuality, the kit format saves money and resources for everyone by dramatically reducing waste. 2) The other service provided in a kit is quality control" (page 39, column 1).

Conclusion

No claims are allowed.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Samuel Woolwine whose telephone number is (571) 272-1144. The examiner can normally be reached on Mon-Fri 9:00am-5:00pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Gary Benzion can be reached on (571) 272-0782. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

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